

Camille Scott

Permanent Address

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(as of July 2020)

EDUCATION	Alma College , Alma, MI <i>B.S., Computer Science</i>	2008-2012
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	Michigan State University , East Lansing, MI <i>DIB Lab, PhD. student, Computer Science</i>	2012-2015
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	University of California Davis , Davis, CA <i>DIB Lab, PhD. student, Computer Science</i>	2015-2022
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HONOURS AND AWARDS	National Merit Finalist	2008
	Alma College / Distinguished Scholar Award	2008-2012
	Binghamton University / Research Experience for Undergrads	2011
	USDA / MSU / National Needs Fellow	2013-2015

MANUSCRIPTS	Reiter, T., Brooks, P. T., Irber, L., Joslin, S. E., Reid, C. M., Scott, C., ... & Pierce, N. T. (2020). <i>Streamlining Data-Intensive Biology With Workflow Systems..</i> BioRxiv.
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Neches, R. Y., & Scott, C. (2018). *SuchTree: Fast, thread-safe computations with phylogenetic trees.* Journal of Open Source Software, 3(26), 678.

Scott, C. (2017). *shmlast: An improved implementation of Conditional Reciprocal Best Hits with LAST and Python.* The Journal of Open Source Software, 2017.

Ren, J., Chung-Davidson, Y. W., Yeh, C. Y., Scott, C., Brown, T., & Li, W. (2015). *Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey.* BMC genomics, 16(1), 436.

Crusoe, M. R. et. al. (2015). *The khmer software package: enabling efficient nucleotide sequence analysis.* F1000Research, 4.

Aleksic, J., Alexa, A., Attwood, T. K., Hong, N. C., Dahlö, M., Davey, R., ..., & Lahti, L. (2014) *The open science peer review oath.* F1000Research, 3.

BLOGS AND SOCIAL MEDIA	Professional blog at: camillescott.org
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Twitter: @camille_codon

Github: github.com/camillescott

PROFESSIONAL ACTIVITIES	Teaching Assistant (TA) at Alma College , <i>Intro to Computer Science</i>	2011-2012
	Co-founder, Alma College Association for Computing Machinery	2012
	Lead Instructor/TA at Michigan State University , <i>CSE 101</i>	Fall 2012
	Presenter at Michigan State University , <i>Summer Research Opportunities (SROP) Workshop</i>	5/2013
	TA for workshop at Marine Biological Laboratory , <i>Strategies and Techniques for Analyzing Microbial Population Structures</i>	8/2013
	TA for workshop at California Institute of Technology , <i>Workshop on Microbial Bioinformatics</i>	10/2013
	TA for SROP Workshop at Michigan State University , <i>Statistics Bootcamp</i>	05/2014
	Participant in Workshop at The Genome Analysis Center (TGAC) , <i>AllBio Open Science & Reproducibility Best Practices Workshop</i>	09/2014
	Participant in Workshop at University of California Davis , <i>Software Carpentry "Train the Trainers"</i>	01/2015
	Contributor to khmer Protocols Project , <i>Protocols for cloud-based de novo RNA-seq and metagenomic analyses</i> khmer-protocols.readthedocs.org	
	Contributor to open source khmer software package , <i>k-mer counting, graph traversal, and sequence processing</i> github.com/dib-lab/khmer	
	Author and maintainer of goetia , <i>C++ and Python library and command line tools for streaming sequence analysis</i> github.com/camillescott/goetia	
	Author and maintainer of debruijnal-enhance-o-tron , <i>pytest fixtures for random de Bruijn graph generation</i> github.com/camillescott/debruijnal-enhance-o-tron	
	Author and maintainer of dammit , <i>a tool for easy de novo transcriptome annotation</i> github.com/camillescott/dammit	
	Author and maintainer of shmlast , <i>an implementation of conditional reciprocal best hits with Python and LAST</i> github.com/camillescott/shmnlst	

REFERENCES (*Contact details available upon request*)